

#10



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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/828,068

DATE: 04/25/2002
TIME: 15:01:22

Input Set : A:\18941-14.app
Output Set: N:\CRF3\04252002\I828068.raw

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3 <110> APPLICANT: Moon, Yong-Hwan
 4 Chen, Lingjing
 5 Sung, Zinmay R.
 7 <120> TITLE OF INVENTION: NUCLEIC ACIDS THAT CONTROL REPRODUCTIVE DEVELOPMENT IN
 8 PLANTS
 10 <130> FILE REFERENCE: 018941-001400US
 12 <140> CURRENT APPLICATION NUMBER: 09/828,068
 C--> 13 <141> CURRENT FILING DATE: 2002-04-11
 15 <160> NUMBER OF SEQ ID NOS: 2
 17 <170> SOFTWARE: PatentIn Ver. 2.1
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 3896
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Oryza sativa
 24 <220> FEATURE:
 25 <221> NAME/KEY: CDS
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 35 tggatgtgc ctggctgtg ctggctgtgtt gttgattctc tcctcgctgtt ggtgatcgat 240
 37 atg gag att gtt gca gta gat cag gag gga gct cgt gtt gtt ggg acg 288
 38 Met Glu Ile Val Ala Val Asp Gln Glu Gly Ala Arg Val Val Gly Thr
 39 1 5 10 15
 41 aac tgt atg ctt gct cgt ggt gga act ggt gct gta gcg cca gtg ttg 336
 42 Asn Cys Met Leu Ala Arg Gly Gly Thr Gly Ala Val Ala Pro Val Leu
 43 20 25 30
 45 gag ctg aca gcg acg cct cgt cag gat gca gcc gct gaa gct ggt gta 384
 46 Glu Leu Thr Ala Thr Pro Arg Gln Asp Ala Ala Glu Ala Gly Val
 47 35 40 45
 49 gac gaa ccg gca caa cac caa tgc gag cat ttc tcc ata aga ggg tat 432
 50 Asp Glu Pro Ala Gln His Gln Cys Glu His Phe Ser Ile Arg Gly Tyr
 51 50 55 60
 53 gtt gct ctt ctt cag aag gat cca aaa ttc tgc tct cta tct cgg 480
 54 Val Ala Leu Leu Gln Lys Lys Asp Pro Lys Phe Cys Ser Leu Ser Arg
 55 65 70 75 80
 57 att ttc cat gac cag aaa aaa tgt gat gaa cac aaa gct agt tca agc 528
 58 Ile Phe His Asp Gln Lys Lys Cys Asp Glu His Lys Ala Ser Ser Ser
 59 85 90 95
 61 cca ttt tct gta gca aag ttt cga cga tgg gat tgc tcg aag tgc ttg 576
 62 Pro Phe Ser Val Ala Lys Phe Arg Arg Trp Asp Cys Ser Lys Cys Leu
 63 100 105 110

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67								115			120				125		
69	gca	aag	cag	aat	ggc	aca	agt	gat	ggt	tgc	tcc	atc	aca	ttt	gtt	cgg	672
70	Ala	Lys	Gln	Asn	Gly	Thr	Ser	Asp	Gly	Cys	Ser	Ile	Thr	Phe	Val	Arg	
71								130			135			140			
73	agc	act	ttt	gtg	cct	gct	agt	gat	ggt	tcc	caa	aaa	gtg	tct	cct	agc	720
74	Ser	Thr	Phe	Val	Pro	Ala	Ser	Val	Gly	Ser	Gln	Lys	Val	Ser	Pro	Ser	
75	145							150			155			160			
77	aca	caa	tca	tct	caa	ggg	aag	aat	gct	gat	aga	tca	act	ctt	cca	aag	768
78	Thr	Gln	Ser	Ser	Gln	Gly	Lys	Asn	Ala	Asp	Arg	Ser	Thr	Leu	Pro	Lys	
79								165			170			175			
81	agt	gtg	caa	gaa	ggc	aat	gac	tcc	aaa	tgc	aat	gcg	cct	tct	ggc	aag	816
82	Ser	Val	Gln	Glu	Gly	Asn	Asp	Ser	Lys	Cys	Asn	Ala	Pro	Ser	Gly	Lys	
83								180			185			190			
85	aat	gga	gct	gag	gcc	aat	act	gat	tca	cca	atg	aaa	gat	ttg	caa		864
86	Asn	Gly	Ala	Ala	Glu	Ala	Asn	Thr	Asp	Ser	Pro	Met	Lys	Asp	Leu	Gln	
87								195			200			205			
89	ggg	cca	gcc	caa	aat	tat	gat	gtg	gca	gca	aat	gtc	tct	gag	gac	aac	912
90	Gly	Pro	Ala	Gln	Asn	Tyr	Asp	Val	Ala	Ala	Asn	Val	Ser	Glu	Asp	Asn	
91								210			215			220			
93	act	tct	gtt	gat	gtt	ggg	gct	tta	cct	gaa	gtt	ccc	cag	att	aca	tgg	960
94	Thr	Ser	Val	Asp	Val	Gly	Ala	Leu	Pro	Glu	Val	Pro	Gln	Ile	Thr	Trp	
95	225							230			235			240			
97	cac	ata	gaa	gta	aat	ggt	gca	gat	caa	cct	tcc	act	cca	aaa	ctt		1008
98	His	Ile	Glu	Val	Asn	Gly	Ala	Asp	Gln	Pro	Pro	Ser	Thr	Pro	Lys	Leu	
99								245			250			255			
101	tct	gaa	gtg	gtc	ctc	aaa	aga	aat	gaa	gat	gaa	aat	gga	aaa	act	gaa	1056
102	Ser	Glu	Val	Val	Leu	Lys	Arg	Asn	Glu	Asp	Glu	Asn	Gly	Lys	Thr	Glu	
103								260			265			270			
105	gag	act	ctt	gtt	gct	gag	cag	tgc	aat	ttg	acc	aaa	gat	cct	aac	cca	1104
106	Glu	Thr	Leu	Val	Ala	Glu	Gln	Cys	Asn	Leu	Thr	Lys	Asp	Pro	Asn	Pro	
107								275			280			285			
109	atg	tct	gga	aag	gaa	cgt	gat	cag	gtt	gct	gag	cag	tgc	aat	ttg	acc	1152
110	Met	Ser	Gly	Lys	Glu	Arg	Asp	Gln	Val	Ala	Glu	Gln	Cys	Asn	Leu	Thr	
111								290			295			300			
113	aaa	gat	ccg	aaa	cca	gtg	tct	ggg	cag	aaa	tgt	gag	cag	atc	tgc	aat	1200
114	Lys	Asp	Pro	Lys	Pro	Val	Ser	Gly	Gln	Lys	Cys	Glu	Gln	Ile	Cys	Asn	
115	305							310			315			320			
117	gag	cca	tgt	gaa	gaa	gtt	gtt	ctc	aaa	aga	agc	tcc	aaa	tct	aag	agg	1248
118	Glu	Pro	Cys	Glu	Glu	Val	Val	Leu	Lys	Arg	Ser	Ser	Lys	Ser	Lys	Arg	
119								325			330			335			
121	aag	acg	gat	aag	aag	ttg	atg	aag	aag	cag	cag	cac	agc	aag	aaa	cgc	1296
122	Lys	Thr	Asp	Lys	Lys	Leu	Met	Lys	Lys	Gln	Gln	His	Ser	Lys	Lys	Arg	
123								340			345			350			
125	act	gcc	cag	gct	gat	gtt	tca	gat	gca	aag	ctt	tgt	cgg	aga	aag	cca	1344
126	Thr	Ala	Gln	Ala	Asp	Val	Ser	Asp	Ala	Lys	Leu	Cys	Arg	Arg	Lys	Pro	
127								355			360			365			
129	aaa	aag	gtg	cgg	ctt	cta	tca	gaa	att	ata	aat	gct	aac	cag	gtt	gag	1392

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134	Asp Ser Arg Ser Asp Glu Val His Arg Glu Asn Ala Ala Asp Pro Cys			
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137	gag gat gat aga agt acc atc ccg gtc ccg atg gaa gta agc atg gat	1488		
138	Glu Asp Asp Arg Ser Thr Ile Pro Val Pro Met Glu Val Ser Met Asp			
139	405	410	415	
141	att cct gtt agc aac cat aca gtg gga gaa gat ggg tta aaa tca agt	1536		
142	Ile Pro Val Ser Asn His Thr Val Gly Glu Asp Gly Leu Lys Ser Ser			
143	420	425	430	
145	aag aac aag aca aaa cgc aaa tac tct gat gtt gta gat gat gga tca	1584		
146	Lys Asn Lys Thr Lys Arg Lys Tyr Ser Asp Val Val Asp Asp Gly Ser			
147	435	440	445	
149	tca ctt atg aac tgg ctg aat gga aaa aag aaa aga act gga agt gtg	1632		
150	Ser Leu Met Asn Trp Leu Asn Gly Lys Lys Arg Thr Gly Ser Val			
151	450	455	460	
153	cat cac aca gtt cat cca gct ggg aat ttg agc aac aaa aaa gtg	1680		
154	His His Thr Val Ala His Pro Ala Gly Asn Leu Ser Asn Lys Lys Val			
155	465	470	475	480
157	aca ccc act gcg agt act cag cat gat gat gag aat gat act gaa aat	1728		
158	Thr Pro Thr Ala Ser Thr Gln His Asp Asp Glu Asn Asp Thr Glu Asn			
159	485	490	495	
161	ggt ctt gac aca aat atg cat aag aca gat gtc tgt cag cat gta tca	1776		
162	Gly Leu Asp Thr Asn Met His Lys Thr Asp Val Cys Gln His Val Ser			
163	500	505	510	
165	gaa atc tcc aca cag agg tgc tca tca aag ggg aaa aca gcg ggt ttg	1824		
166	Glu Ile Ser Thr Gln Arg Cys Ser Ser Lys Gly Lys Thr Ala Gly Leu			
167	515	520	525	
169	agt aag ggg aaa aca cat tca gct gct agt acc aaa tat ggt ggt gaa	1872		
170	Ser Lys Gly Lys Thr His Ser Ala Ala Ser Thr Lys Tyr Gly Gly Glu			
171	530	535	540	
173	agc acc aga aat ggt cag aac ata cat gta ctc agc gca gaa gat caa	1920		
174	Ser Thr Arg Asn Gly Gln Asn Ile His Val Leu Ser Ala Glu Asp Gln			
175	545	550	555	560
177	tgc cag atg gaa acc gaa aac tct gtt ctg agt cac tcg gca aag gtt	1968		
178	Cys Gln Met Glu Thr Glu Asn Ser Val Leu Ser His Ser Ala Lys Val			
179	565	570	575	
181	tct cca gct gag cat gat atc caa att atg tct gac ctt cat gag cag	2016		
182	Ser Pro Ala Glu His Asp Ile Gln Ile Met Ser Asp Leu His Glu Gln			
183	580	585	590	
185	agt cta ccc aag aag aaa aag caa aaa ctt gaa gtg act cgt gaa	2064		
186	Ser Leu Pro Lys Lys Lys Lys Gln Lys Leu Glu Val Thr Arg Glu			
187	595	600	605	
189	aaa cag acc atg ata gat gac atc ccc atg gat att gtt gaa ctg cta	2112		
190	Lys Gln Thr Met Ile Asp Asp Ile Pro Met Asp Ile Val Glu Leu Leu			
191	610	615	620	
193	gct aaa aac cag cat gag agg cag ctt atg act gag act gat tgt tct	2160		
194	Ala Lys Asn Gln His Glu Arg Gln Leu Met Thr Glu Thr Asp Cys Ser			

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201	ata gta gct gcc aag gat ggt tca gat tat gca tca agt gtg ttt gac				2256
202	Ile Val Ala Ala Lys Asp Gly Ser Asp Tyr Ala Ser Ser Val Phe Asp				
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205	act aat tcc caa cag aag tcc ttg gca tcc caa agt aca cag aag gag				2304
206	Thr Asn Ser Gln Gln Lys Ser Leu Ala Ser Gln Ser Thr Gln Lys Glu				
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209	tta cag ggt cat ttg gca ttg acc aca caa gag tct cca cat cct cag				2352
210	Leu Gln Gly His Leu Ala Leu Thr Thr Gln Glu Ser Pro His Pro Gln				
211	690	695	700		
213	aac ttt cag tct act cag gaa cag cag aca cat ttg cgg atg gaa gaa				2400
214	Asn Phe Gln Ser Thr Gln Glu Gln Gln Thr His Leu Arg Met Glu Glu				
215	705	710	715	720	
217	atg gtc act att gct gca agc tca cca cta ttg tca cat cat gat gat				2448
218	Met Val Thr Ile Ala Ala Ser Ser Pro Leu Phe Ser His His Asp Asp				
219	725	730	735		
221	cag tat att gct gaa gca cca act gaa cat ttg ggc cgt aag gac gca				2496
222	Gln Tyr Ile Ala Glu Ala Pro Thr Glu His Trp Gly Arg Lys Asp Ala				
223	740	745	750		
225	aag aag cta acg ttg gag caa ttt aag gcc act aca aga aat tct cca				2544
226	Lys Lys Leu Thr Trp Glu Gln Phe Lys Ala Thr Thr Arg Asn Ser Pro				
227	755	760	765		
229	gca gca aca tgt ggt gct caa ttt aga cct ggt atc caa gca gtt gac				2592
230	Ala Ala Thr Cys Gly Ala Gln Phe Arg Pro Gly Ile Gln Ala Val Asp				
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234	Leu Thr Ser Thr His Val Met Gly Ser Ser Asn Tyr Ala Ser Arg				
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237	caa cca gta att gcg cca ctg gac cgc tat gct gaa aga gcg gtt aac				2688
238	Gln Pro Val Ile Ala Pro Leu Asp Arg Tyr Ala Glu Arg Ala Val Asn				
239	805	810	815		
241	cag gtc cat gca aga aat ttt cca agc aca ata gca acc atg gaa gcg				2736
242	Gln Val His Ala Arg Asn Phe Pro Ser Thr Ile Ala Thr Met Glu Ala				
243	820	825	830		
245	agt aag tta tgt gat cgg aga aat gct gga caa gta gtc ttg tat cct				2784
246	Ser Lys Leu Cys Asp Arg Arg Asn Ala Gly Gln Val Val Leu Tyr Pro				
247	835	840	845		
249	aaa gaa tcc atg cct gcg acg cat ctt ctg aga atg atg gat cca tca				2832
250	Lys Glu Ser Met Pro Ala Thr His Leu Leu Arg Met Met Asp Pro Ser				
251	850	855	860		
253	aca tta gca agc ttc ccc aac tat gga act tct agc agg aac cag atg				2880
254	Thr Leu Ala Ser Phe Pro Asn Tyr Gly Thr Ser Arg Asn Gln Met				
255	865	870	875	880	
257	gag tct caa ctt cat aat tct cag tat gca cat aat cag tac aaa gga				2928
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265	aca ttc gaa gac tta tca cgg cat cag ctg cat gat ctg cac aga cct	3024
266	Thr Phe Glu Asp Leu Ser Arg His Gln Leu His Asp Leu His Arg Pro	
267	915 920 925	
269	tta cgc cca cat cct aga gtt ggt gtg ctt ggc tcc ttg ctg cag aag	3072
270	Leu Arg Pro His Pro Arg Val Gly Val Leu Gly Ser Leu Leu Gln Lys	
271	930 935 940	
273	gaa att gca aac tgg tcg gag aac tgt ggc aca caa tct ggt tat aag	3120
274	Glu Ile Ala Asn Trp Ser Glu Asn Cys Gly Thr Gln Ser Gly Tyr Lys	
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277	tta gga gtg tca aca gga ata aca tcg cat cag atg aac aga aag gaa	3168
278	Leu Gly Val Ser Thr Gly Ile Thr Ser His Gln Met Asn Arg Lys Glu	
279	965 970 975	
281	cat ttt gaa gcc ctg aat tct gga atg ttt tca gca aaa tgg aat gca	3216
282	His Phe Glu Ala Leu Asn Ser Gly Met Phe Ser Ala Lys Trp Asn Ala	
283	980 985 990	
285	ttg cag ttg ggt tct gtt agc tcc agt gca gat ttt tta tca gcg agg	3264
286	Leu Gln Leu Gly Ser Val Ser Ser Ala Asp Phe Leu Ser Ala Arg	
287	995 1000 1005	
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291	1010 1015 1020	
293	ccc ttg gat cgg ttt gtg aga cag gat atc tgt ata act aac aag aac	3360
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314	agctgtgtgt gactgacggc gagaaatggg tttgtcggtg ttaaggttga aacgactagc	3821
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331	20 25 30	

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